SEQUENCE LISTING

<110> AVENTIS PHARMA SA
      US GOVERNMENT of the UNITED STATES

<120> NUCLEIC ACID OF THE HUMAN ABCC11 GENE, VECTORS
      CONTAINING SUCH NUCLEIC ACID, AND USES THEREOF

<130> ABCC11 GENE

<140> ST01005
<141> 2002-03-05

<150> 60/272,757
<151> 2001-03-05

<160> 31

<170> PatentIn Ver. 2.1

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<213> Homo sapiens

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Asn Pro Glu Ala Pro Gly Arg Ala Ala Val Pro Pro Trp Gly Lys Tyr
        50   55   60

Asp Ala Ala Leu Arg Thr Met Ile Pro Phe Arg Pro Lys Pro Arg Phe
65   70   75   80

Pro Ala Pro Gln Pro Leu Asp Asn Ala Gly Leu Phe Ser Tyr Leu Thr
                85   90   95

Val Ser Trp Leu Thr Pro Leu Met Ile Gln Ser Leu Arg Ser Arg Leu
                100   105   110

Asp Glu Asn Thr Ile Pro Pro Leu Ser Val His Asp Ala Ser Asp Lys
            115   120   125

Asn Val Gln Arg Leu His Arg Leu Trp Glu Glu Glu Val Ser Arg Arg
        130   135   140

Gly Ile Glu Lys Ala Ser Val Leu Leu Val Met Leu Arg Phe Gln Arg
145   150   155   160

Thr Arg Leu Ile Phe Asp Ala Leu Leu Gly Ile Cys Phe Cys Ile Ala
                165   170   175

Ser Val Leu Gly Pro Ile Leu Ile Ile Pro Lys Ile Leu Glu Tyr Ser
                180   185   190

Glu Glu Gln Leu Gly Asn Val Val His Gly Val Gly Leu Cys Phe Ala
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Leu Phe Leu Ser Glu Cys Val Lys Ser Leu Ser Phe Ser Ser Ser Trp
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225   230   235   240

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Lys Met Tyr Thr Trp Glu Lys Pro Phe Ala Lys Ile Ile Glu Asp Leu
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Trp Val Leu Ile His Thr Ser Leu Lys Leu Lys Leu Thr Ala Ser Met
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Ala Phe Ser Met Leu Ala Ser Leu Asn Leu Leu Arg Leu Ser Val Phe
            420             425              430

Phe Val Pro Ile Ala Val Lys Gly Leu Thr Asn Ser Lys Ser Ala Val
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Met Arg Phe Lys Lys Phe Phe Leu Gln Glu Ser Pro Val Phe Tyr Val
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Gln Thr Leu Gln Asp Pro Ser Lys Ala Leu Val Phe Glu Glu Ala Thr
465             470             475              480

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            485             490              495

Leu Glu Arg Asn Gly His Ala Ser Glu Gly Met Thr Arg Pro Arg Asp
            500             505             510

Ala Leu Gly Pro Glu Glu Glu Gly Asn Ser Leu Gly Pro Glu Leu His
            515             520             525

Lys Ile Asn Leu Val Val Ser Lys Gly Met Met Leu Gly Val Cys Gly
    530             535             540

Asn Thr Gly Ser Gly Lys Ser Ser Leu Leu Ser Ala Ile Leu Glu Glu
545             550             555             560
```

Met His Leu Leu Glu Gly Ser Val Gly Val Gln Gly Ser Leu Ala Tyr
                565   570   575

Val Pro Gln Gln Ala Trp Ile Val Ser Gly Asn Ile Arg Glu Asn Ile
            580   585   590

Leu Met Gly Gly Ala Tyr Asp Lys Ala Arg Tyr Leu Gln Val Leu His
        595   600   605

Cys Cys Ser Leu Asn Arg Asp Leu Glu Leu Leu Pro Phe Gly Asp Met
    610   615   620

Thr Glu Ile Gly Glu Arg Gly Leu Asn Leu Ser Gly Gly Gln Lys Gln
625   630   635   640

Arg Ile Ser Leu Ala Arg Ala Val Tyr Ser Asp Arg Gln Ile Tyr Leu
            645   650   655

Leu Asp Asp Pro Leu Ser Ala Val Asp Ala His Val Gly Lys His Ile
            660   665   670

Phe Glu Glu Cys Ile Lys Lys Thr Leu Arg Gly Lys Thr Val Val Leu
        675   680   685

Val Thr His Gln Leu Gln Tyr Leu Glu Phe Cys Gly Gln Ile Ile Leu
    690   695   700

Leu Glu Asn Gly Lys Ile Cys Glu Asn Gly Thr His Ser Glu Leu Met
705   710   715   720

Gln Lys Lys Gly Lys Tyr Ala Gln Leu Ile Gln Lys Met His Lys Glu
            725   730   735

Ala Thr Ser Asp Met Leu Gln Asp Thr Ala Lys Ile Ala Glu Lys Pro
            740   745   750

Lys Val Glu Ser Gln Ala Leu Ala Thr Ser Leu Glu Glu Ser Leu Asn
        755   760   765

Gly Asn Ala Val Pro Glu His Gln Leu Thr Gln Glu Glu Glu Met Glu
    770   775   780

Glu Gly Ser Leu Ser Trp Arg Val Tyr His His Tyr Ile Gln Ala Ala
785   790   795   800

Gly Gly Tyr Met Val Ser Cys Ile Ile Phe Phe Phe Val Val Leu Ile
            805   810   815

Val Phe Leu Thr Ile Phe Ser Phe Trp Trp Leu Ser Tyr Trp Leu Glu
            820   825   830

Gln Gly Ser Gly Thr Asn Ser Ser Arg Glu Ser Asn Gly Thr Met Ala
        835   840   845

Asp Leu Gly Asn Ile Ala Asp Asn Pro Gln Leu Ser Phe Tyr Gln Leu
    850   855   860

Val Tyr Gly Leu Asn Ala Leu Leu Leu Ile Cys Val Gly Val Cys Ser
865   870   875   880

Ser Gly Ile Phe Thr Lys Val Thr Arg Lys Ala Ser Thr Ala Leu His

885   890   895

Asn Lys Leu Phe Asn Lys Val Phe Arg Cys Pro Met Ser Phe Phe Asp
            900   905   910

Thr Ile Pro Ile Gly Arg Leu Leu Asn Cys Phe Ala Gly Asp Leu Glu
            915   920   925

Gln Leu Asp Gln Leu Leu Pro Ile Phe Ser Glu Gln Phe Leu Val Leu
        930   935   940

Ser Leu Met Val Ile Ala Val Leu Leu Ile Val Ser Val Leu Ser Pro
945   950   955   960

Tyr Ile Leu Leu Met Gly Ala Ile Ile Met Val Ile Cys Phe Ile Tyr
                965   970   975

Tyr Met Met Phe Lys Lys Ala Ile Gly Val Phe Lys Arg Leu Glu Asn
            980   985   990

Tyr Ser Arg Ser Pro Leu Phe Ser His Ile Leu Asn Ser Leu Gln Gly
        995   1000   1005

Leu Ser Ser Ile His Val Tyr Gly Lys Thr Glu Asp Phe Ile Ser Gln
    1010   1015   1020

Phe Lys Arg Leu Thr Asp Ala Gln Asn Asn Tyr Leu Leu Leu Phe Leu
1025   1030   1035   1040

Ser Ser Thr Arg Trp Met Ala Leu Arg Leu Glu Ile Met Thr Asn Leu
            1045   1050   1055

Val Thr Leu Ala Val Ala Leu Phe Val Ala Phe Gly Ile Ser Ser Thr
        1060   1065   1070

Pro Tyr Ser Phe Lys Val Met Ala Val Asn Ile Val Leu Gln Leu Ala
        1075   1080   1085

Ser Ser Phe Gln Ala Thr Ala Arg Ile Gly Leu Glu Thr Glu Ala Gln
    1090   1095   1100

Phe Thr Ala Val Glu Arg Ile Leu Gln Tyr Met Lys Met Cys Val Ser
1105   1110   1115   1120

Glu Ala Pro Leu His Met Glu Gly Thr Ser Cys Pro Gln Gly Trp Pro
            1125   1130   1135

Gln His Gly Glu Ile Ile Phe Gln Asp Tyr His Met Lys Tyr Arg Asp
            1140   1145   1150

Asn Thr Pro Thr Val Leu His Gly Ile Asn Leu Thr Ile Arg Gly His
        1155   1160   1165

Glu Val Val Gly Ile Val Gly Arg Thr Gly Ser Gly Lys Ser Ser Leu
    1170   1175   1180

Gly Met Ala Leu Phe Arg Leu Val Glu Pro Met Ala Gly Arg Ile Leu
1185   1190   1195   1200

Ile Asp Gly Val Asp Ile Cys Ser Ile Gly Leu Glu Asp Leu Arg Ser
            1205   1210   1215

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Lys Leu Ser Val Ile Pro Gln Asp Pro Val Leu Leu Ser Gly Thr Ile
         1220             1225             1230

Arg Phe Asn Leu Asp Pro Phe Asp Arg His Thr Asp Gln Gln Ile Trp
         1235             1240             1245

Asp Ala Leu Glu Arg Thr Phe Leu Thr Lys Ala Ile Ser Lys Phe Pro
     1250             1255             1260

Lys Lys Leu His Thr Asp Val Val Glu Asn Gly Gly Asn Phe Ser Val
1265             1270             1275             1280

Gly Glu Arg Gln Leu Leu Cys Ile Ala Arg Ala Val Leu Arg Asn Ser
             1285             1290             1295

Lys Ile Ile Leu Ile Asp Glu Ala Thr Ala Ser Ile Asp Met Glu Thr
         1300             1305             1310

Asp Thr Leu Ile Gln Arg Thr Ile Arg Glu Ala Phe Gln Gly Cys Thr
         1315             1320             1325

Val Leu Val Ile Ala His Arg Val Thr Thr Val Leu Asn Cys Asp His
     1330             1335             1340

Ile Leu Val Met Gly Asn Gly Lys Val Val Glu Phe Asp Arg Pro Glu
1345             1350             1355             1360

Val Leu Arg Lys Lys Pro Gly Ser Leu Phe Ala Ala Leu Met Ala Thr
             1365             1370             1375

Ala Thr Ser Ser Leu Arg
         1380
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Sequence Comparison "A"

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LOCUS         AI676121              326 bp    mRNA     linear    EST 17-DEC-1999
DEFINITION    wc05f11.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2314317 3',
              mRNA sequence.
ACCESSION     AI676121
VERSION       AI676121.1  GI:4876601
KEYWORDS      EST.
SOURCE        human.
  ORGANISM    Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE     1  (bases 1 to 326)
  AUTHORS     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE       National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
              Tumor Gene Index
  JOURNAL     Unpublished (1997)
COMMENT       Contact: Robert Strausberg, Ph.D.
              Email: cgapbs-r@mail.nih.gov
              Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
              Emmert-Buck, M.D., Ph.D.
               cDNA Library Preparation: M. Bento Soares, Ph.D.
               cDNA Library Arrayed by: Greg Lennon, Ph.D.
              DNA Sequencing by: Washington University Genome Sequencing Center
               Clone distribution: NCI-CGAP clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              www-bio.llnl.gov/bbrp/image/image.html
              Insert Length: 295   Std Error: 0.00
              Seq primer: -40UP from Gibco.
FEATURES             Location/Qualifiers
     source          1. .326
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2314317"
                     /clone_lib="NCI_CGAP_Pr28"
                     /sex="male"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /note="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia)
                     with a modified polylinker; Plasmid DNA from the
                     normalized library NCI_CGAP_Pr22 was prepared, and ss
                     circles were made in vitro. Following HAP purification,
                     this DNA was used as tracer in a subtractive hybridization
                     reaction. The driver was PCR-amplified cDNAs from a pool
                     of 5,000 clones made from the same library (cloneIDs
                     985608-986759, 1101192-1101959, and 1217928-1220615).
                     Subtraction by Bento Soares and M. Fatima Bonaldo.  "
BASE COUNT        94 a     81 c  .  61 g      90 t
ORIGIN
```

```
Query Match                6.4%;  Score 310.2;  DB 9;  Length 326;
Best Local Similarity     99.0%;  Pred. No. 1.2e-78;
Matches  312;  Conservative   0;  Mismatches   3;  Indels   0;  Gaps   0;
```

```
Qy    4540 GAGGTTCACACAGGTGCAGCTTCGAGGCCCACAGTCTGCGACCTTCTTGTTTGGAGATGA 4599
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     326 GAGGTTCACACAGGTGCAGCTTCGAGGCCCACAGTCTGCGACCTTCTTGTTTGGAGATGA 267

Qy    4600 GAACTTCTCCTGGAAGCAGGGGTAAATGTAGGGGGGGGTGGGGATTGCTGGATGGAAACCC 4659
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db     266 GAACTTCTCCTGGAAGCAGGGGTAAATGTAGGGGGGGGTGGGGATTGCTGGATGGAACCCC 207

Qy    4660 TGGAATAGGCTACTTGATGGCTCTCAAGACCTTAGAACCCCAGAACCATCTAAGACATGG 4719
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     206 TGGAATAGGCTACTTGATGGCTCTCAAGACCTTAGAACCCCAGAACCATCTAAGACATGG 147

Qy    4720 GATTCAGTGATCATGTGGTTCTCCTTTTAACTTACATGCTGAATAATTTTATAATAAGGT 4779
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     146 GATTCAGTGATCATGTGGTTCTCCTTTTAACTTACATGCTGAATAATTTTATAATAAGGT 87

Qy    4780 AAAAGCTTATAGTTTTCTGATCTGTGTTAGAAGTGTTGCAAATGCTGTACTGACTTTGTA 4839
           |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db      86 AAAAGCTTATAGTTTTCTGATCTGTGTTAGAAGTGTTGCAAATGCTGTACCCACTTTGTA 27

Qy    4840 AAATATAAAACTAAG 4854
           |||||||||||||||
Db      26 AAATATAAAACTAAG 12
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